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To: "Harold Varmus" <Harold\_Varmus@nih.gov>,  
"Pat Brown" <pbrown@cmgm.stanford.edu>  
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Given the exchange with Nick I thought it'd be useful to state explicitly my understanding of what it means to be "in E-BioSci".

What does it mean to be "in E-Biosci"?

The essential concept of E-BioSci is the creation of a central repository for primary life science research - both peer-reviewed and screened submissions. Articles in the central repository would be open for searching, viewing, linking in & out, and there would be a commitment for archiving. Features of articles within E-BioSci - aspects of presentation, links, functionality, etc. - would be determined through input by users and a formal advisory board. Participating publishers would be an important source of this input but their approval would not be required to institute these changes. Within reasonable constraints, efforts would be made to satisfy the desires of a given publisher to distinguish their content without impacting overall functionality.

The most important variable in the relationship a journal might have with E-BioSci is the delay of submission from publication date. Some journals would immediately submit articles to E-BioSci upon acceptance, while others might impose e.g. a several month delay. While some journals might maintain their own websites and request links back to content on their site, others may not - and this has an insignificant consequence on the functionality of E-BioSci.

To put it simply, if a journal is "in E-BioSci", then it is fully accessible regardless of the delay. If a journal wants to provide free access to content on their website (as does BMJ and JCI, and a number of others with back content), that is a good thing. But it is not in E-BioSci if it's not accessible within E-BioSci. Contorting the concept of a central repository to one of links instead of content is not productive. Imagine if the sequence database evolved that way?

David